

SEQ ID NO:23

AB005659
LOCUS AB005659 4939 bp mRNA PRI 21-OCT-1997
DEFINITION Homo sapiens SMRP mRNA, complete cds.
ACCESSION AB005659
VERSION AB005659.1 GI:2554609
KEYWORDS SMRP.
SOURCE Homo sapiens bone marrow cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4939)
AUTHORS Suzuki, T.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1997) to the DDBJ/EMBL/GenBank databases.
Toshihiro Suzuki, National Cancer Center Research Institute,
Pharmacology Division; Tsukiji 5-1-1, Chuo-ku, Tokyo 104, Japan
(E-mail:tssuzuki@gan2.res.ncc.go.jp, Tel:03-3542-2511,
Fax:03-3542-1886)
REFERENCE 2 (sites)
AUTHORS Suzuki, T., Nishio, K., Sasaki, H., Kurokawa, H., Saito-Ohara, F.,
Ikeuchi, T., Tanabe, S., Terada, M. and Saijo, N.
TITLE cDNA cloning of a short type of multidrug resistance protein
homologue, SMRP, from a human lung cancer cell line
JOURNAL Biochem. Biophys. Res. Commun. 238 (3), 790-794 (1997)
MEDLINE 97472289
FEATURES Location/Qualifiers
source 1. .4939
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3q27"
/tissue_type="bone marrow"
gene 737. .3577
/gene="SMRP"
CDS 737. .3577
/gene="SMRP"
/note="a short type of multidrug resistance protein
homologue"
/codon_start=1
/protein_id="BAA22887.1"
/db_xref="GI:2554610"

/translation="MKNATLAWDSSHSSIQNSPKLTPKMKKDKRASRGKKEKVRQLQR
TEHQAVLAEQKGHLLLDSDERPSPEEEEGKHIHLGHLRLQRTLHSIDLEIQEGKLVGI
CGSVGSGKTSLSAILGQMTLLEGSIAISGTFAYVAQQAWILNATLRDNILFGKEYDE
ERYNSVLNCCLRPDLAILPSSDLTEIGERGANLSSGGQRQRISLARALYSRDSIYILD
DPLSALDAHVGNIHFNSAIRKHLKSKTVLTVTHQLQYLVDCEVIFMKEGCITERGTH
EELMNLNGDYATIFNNLLGETPPVEINSKKTSGSQKKSQDKGPKTGSVKKEKAVKP
EEGQLVQLEEKQGQSVFPWSVYGVYIQAGGPLAFLVIMALFMLNVGSAFSTWWLSYW
IKQSGSNTTVTRGNETSVSDSMKDNPHMQYYASIYALSMVMLILKAIRGVVVFVKGTL
RASSRLHDELFRILRSPMKFFDTTPTGRILNRFSKDMDEVDRLPFQAEMFIQNVIL
VFFCVGMIAGVFPWFLVAVGPLVILFSLHIVSRVLIRELKRDLNITQSPFLSHITSS
IQGLATIHAYNKGQEFLLHRYQELLDDNQAPFFLFTCAMRWLAVRLDLISIALITTTGL
MIVLMHGQIPPAYAGLAISYAVQLTGLFQFTVRLASETEARFTSVERINHYIKTSLSE
APARIKNKAPSPDWPQEGEVTFENAEMRYRENLPVLVKVSFTIKPKEKIGIVGRTGS

BEST AVAILABLE COPY

```

polyA_site      4939
                /note="15 A nucleotides"
BASE COUNT      1174 a    1224 c    1249 g    1292 t
ORIGIN

```

```

Query Match          11.6%; Score 425; DB 85; Length 4939;
Best Local Similarity 56.1%; Pred. No. 2.1e-89;
Matches 800; Conservative 0; Mismatches 625; Indels 0; Gaps
0;

```

Qy	2217	ggttttccgctgccccatgagtttcttttgacaccatcccaataggccggcttttgaactg	2276
Db	2125	GATCCTTCGAAGCCCTATGAAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAG	2184
Qy	2277	cttcgcaggggacttggaacagctggaccagctcttgcccatcttttcagagcagttcct	2336
Db	2185	GTTTTCCAAAGACATGGATGAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTTCAT	2244
Qy	2337	ggtcctgtccttaatggtgatcgccgtcctgttgattgtcagtggtgtgtctccatatat	2396
Db	2245	CCAGAACGTTATCCTGGTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTT	2304
Qy	2397	cctgttaatgggagccataatcatggttatttgcctcatttattatatgatgttcaagaa	2456
Db	2305	CCTTGTTGGCAGTGGGGCCCCTTGTTCATCCTCTTTTCAGTCTGCACATTGTCTCCAGGGT	2364
Qy	2457	ggccatcggtgtgtttcaagagactggagaactatagccggtctcctttattctcccat	2516
Db	2365	CCTGATTCGGGAGCTGAAGCGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCACAT	2424
Qy	2517	cctcaattctctgcaaggcctgagctccatccatgtctatggaaaaactgaagacttcat	2576
Db	2425	CACGTCCAGCATACAGGGCCTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCT	2484
Qy	2577	cagccagtttaagaggctgactgatgcgcagaataactacctgctgttgtttctatcttc	2636
Db	2485	GCACAGATACCAGGAGCTGCTGGATGACAACCAAGCTCCTTTTTTTTTTGTTTACGTGTGC	2544
Qy	2637	cacacgatggatggcattgaggctggagatcatgaccaaccttgtgaccttggctgttgc	2696
Db	2545	GATGCGGTGGCTGGCTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGG	2604
Qy	2697	cctgttcgtggcttttggcatttccctccacccccctactcctttaaagtcatggctgtcaa	2756
Db	2605	GCTGATGATCGTTCTTATGCACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTC	2664
Qy	2757	catcgtgctgcagctggcgctccagcttccaggccactgccggattggcttggagacaga	2816
Db	2665	TTATGCTGTCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGA	2724
Qy	2817	ggcacagttcacggctgtagaaagagataactgcagttacatgaaqatgtgtgtctcggaagc	2876

BEST AVAILABLE COPY

Db 2725 AGCTCGATTACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCCCTGGAAGC 2784
 Qy 2877 tcctttacacatggaaggcacaagttgtccccaggggtggccacagcatggggaaatcat 2936
 Db 2785 ACCTGCCAGAATTAAGAACAAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGAC 2844
 Qy 2937 atttcaggattatcacatgaaatacagagacaacacacccaccgtgcttcacggcatcaa 2996
 Db 2845 CTTTGAGAACGCAGAGATGAGGTACCGAGAAAAACCTCCCTCTTGTCTTAAAGAAAGTATC 2904
 Qy 2997 cctgaccatccgcggccacgaagtgggtgggcatcgtgggaaggacgggctctgggaagtc 3056
 Db 2905 CTTCACGATCAAACCTAAAGAGAAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTC 2964
 Qy 3057 ctccttgggcatggctctcttccgcctgggtggagcccatggcaggccggattctcattga 3116
 Db 2965 CTCGCTGGGGATGGCCCTCTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGA 3024
 Qy 3117 cggcgtggacatttgcagcatcggcctggaggacttgcggtccaagctctcagtgatccc 3176
 Db 3025 TGGAGTGAGAATCAGTGATATTGGCCTTGCCGACCTCCGAAGCAAACCTCTCTATCATTC 3084
 Qy 3177 tcaagatccagtgtctgtctcaggaaccatcagattcaacctagatccctttgaccgtca 3236
 Db 3085 TCAAGAGCCGGTGCTGTTTCACTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTA 3144
 Qy 3237 cactgaccagcagatctgggatgccttggagaggacattcctgaccaaggccatctcaaa 3296
 Db 3145 CACTGAAGACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCA 3204
 Qy 3297 gttccccaaaaagctgcatacagatgtggtggaaaacggtggaaacttctctgtggggga 3356
 Db 3205 GCTACCTCTGAAACTTGAATCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGA 3264
 Qy 3357 gaggcagctgtctgtcattgccagggtgtgcttcgcaactccaagatcatccttatcga 3416
 Db 3265 ACGGCAGCTCTTGTGCATAGCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGA 3324
 Qy 3417 tgaagccacagcctccattgacatggagacagacaccctgatccagcgcacaaatccgtga 3476
 Db 3325 TGAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGA 3384
 Qy 3477 agccttccagggtgcaccgtgtctgtcattgcccaccgtgtcaccactgtgtgactg 3536
 Db 3385 AGCATTTCAGACTGTACCATGCTGAACATTGCCCATCGCCTGCACACGGTTCTAGGCTC 3444
 Qy 3537 tgaccacatcctggttatgggcaatgggaagggtgtagaatttgatcggccggagggtact 3596
 Db 3445 CGATAGGATTATGGTGCTGGCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCTC 3504
 Qy 3597 gcggaagaagcctgggtcattgttcgcagccctcatggccacagc 3641
 Db 3505 TCTGTCCAACGACAGTTCCTGATTCTATGCCATGTTTGCTGCTGC 3549

BEST AVAILABLE COPY

THIS PAGE BLANK (USPTO)